

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:33:38 ; Search time 21.5 Seconds  
(without alignments)  
4820.544 Million cell updates/sec

Title: US-10-025-514-16  
Perfect score: 2675  
Sequence: 1 MEDPQGAACKTDTSHHQD.....RLKCCMGCKSCVSPVKA 503

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues 671580

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2027	75.8	418	4 Q96ES1	Q96es1 homo sapien
2	2026	75.7	418	4 Q96BF9	Q96bf9 homo sapien
3	1908	71.3	396	6 O00394	O00394 cercopithec
4	1470	55.0	413	11 O54761	O54761 spermophilu
5	1462.5	54.7	421	6 O46519	O46519 equus cabal
6	1446.5	54.1	413	11 P97277	P97277 mesocricetu
7	1374	51.4	406	11 Q84118	Q84118 meriones un
8	1342	50.2	413	6 Q28665	Q28665 oryctolagus
9	1340	50.1	413	11 Q8VC20	Q8vc20 mus musculu
10	1334	49.9	410	11 Q91WH5	Q91wh5 mus musculu
11	1334	49.9	413	11 Q91X88	Q91x88 mus musculu
12	1334	49.9	413	11 Q91V74	Q91v74 mus musculu
13	1330	49.7	425	11 Q91XC1	Q91xc1 mus musculu
14	1325	49.5	413	6 Q07298	Q07298 oryctolagus
15	1324	49.5	413	11 Q8VC41	Q8vc41 mus musculu
16	1323	49.5	456	6 O62663	O62663 oryctolagus

17	1310	49.0	413	11	O63969	O63969 mus saxicol
18	1307	48.9	413	6	Q28666	Q28666 oryctolagus
19	1290	48.2	413	11	O54762	O54762 spermophilu
20	1184	44.3	413	11	O91X22	O91x22 mus musculu
21	1026	38.4	433	13	O9YIB8	O9yib8 xenopus lae
22	1010	37.8	197	4	Q13747	Q13747 homo sapien
23	849.5	31.8	420	11	O60552	O60552 mesocricetu
24	849	31.7	407	4	Q9UNU9	Q9unu9 homo sapien
25	845	31.6	410	13	O90323	O90323 cyprinus ca
26	829	31.0	418	11	O91X80	O91x80 mus musculu
27	828	31.0	418	11	O8VCH3	O8vch3 mus musculu
28	825	30.8	418	11	O91W80	O91w80 mus musculu
29	820.5	30.7	415	6	O9GMA6	O9gma6 sus scrofa
30	818	30.6	418	11	Q03734	Q03734 mus musculu
31	816	30.5	427	4	O96B25	O96bz5 homo sapien
32	812	30.4	418	11	O62257	O62257 mus musculu
33	811.5	30.3	418	11	O91WP6	O91wp6 mus musculu
34	810.5	30.3	418	11	O62258	O62258 mus musculu
35	794	29.7	404	6	O9N212	O9n212 bos taurus
36	765.5	28.7	406	11	O88292	O88292 rattus norv
37	760	28.4	406	6	O9GK37	O9gk37 sus scrofa
38	758	28.3	411	11	O8R421	O8r421 rattus norv
39	757.5	28.3	415	6	Q27984	Q27984 bos taurus
40	745.5	27.9	418	11	O9D7D2	O9d7d2 mus musculu
41	742	27.7	412	11	O63556	O63556 rattus norv
42	725	27.1	413	11	O9CQ32	O9cq32 mus musculu
43	722.5	27.0	397	11	O91WQ0	O91wq0 mus musculu
44	714	26.7	423	11	P97569	P97569 rattus norv
45	673	25.2	371	6	Q9TTE1	Q9tte1 bos taurus

## ALIGNMENTS

RESULT 1

Q96ES1 ID Q96ES1 PRELIMINARY; PRT; 418 AA.  
AC Q96ES1  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
DE Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1.  
DE Homo sapiens (Human)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
OX [1]  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=OVARY;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR EMBL; BC011991; AAH11991.1;  
DR InterPro; IPR000215; Serpin.  
DR Pfam; PF00079; serpin; 1.  
DR PROSITE; PS00284; SERPIN; UNKNOWN\_1.  
KW Serpin.  
SQ SEQUENCE 418 AA; 46722 MW; 70165484573B7F16 CRC64;

Query Match 75.8%; Score 2027; DB 4; Length 418;  
Best Local Similarity 99.7%; Pred. No. 4.6e-130;  
Matches 393; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EDPOGDAACKTDTSHHQDHPFNKIPNLAEFAFSLYRQLAHQSNSTNFIFFSPVSIATA 61  
Db 25 EDPOGDAACKTDTSHHQDHPFNKIPNLAEFAFSLYRQLAHQSNSTNFIFFSPVSIATA 84  
QY 62 FAMSLSGTADYHDETELEGNLENLFEIPAQIHEGFOELLRTLNQDPSQLQLTGTNGLFL 121  
Db 85 FAMSLSGTADYHDETELEGNLENLFEIPAQIHEGFOELLRTLNQDPSQLQLTGTNGLFL 144  
QY 122 SEGKLVKDFLEDVKLYHSEAFVNFQGTTERAKKQINDYVEKGTQGVKIVDLVKELDRDT 181

Db 145 SGLKLVDFKLEDDVKKLHSAFTVNEGDTEAKKQINDVEGTGQKIVDLVKELDRDT 204  
 QY 182 VFALVNYIFFKQKWERPEVDEEDFHVQDVTVKVPMMKRLGMFNIOHCKKLSWVL 241  
 Db 205 VFALVNYIFFKQKWERPEVDEEDFHVQDVTVKVPMMKRLGMFNIOHCKKLSWVL 264  
 QY 242 LMKYLGNTAIFFLPDGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 301  
 Db 265 LMKYLGNTAIFFLPDGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 324  
 QY 302 SVLGGLGTTKVFNSGADLSGVTEAPLKLKSAVHKAVLTIDKGTGAAGAMFLEAIPMSI 361  
 Db 325 SVLGGLGTTKVFNSGADLSGVTEAPLKLKSAVHKAVLTIDKGTGAAGAMFLEAIPMSI 384  
 QY 362 PPEVKFNKPFVFLMIEQNTKSPFLMGKVVNPQK 395  
 Db 385 PPEVKFNKPFVFLMIDQNTKSPFLMGKVVNPQK 418  
 RESULT 2  
 Q96BF9 PRELIMINARY; PRT; 418 AA.  
 ID Q96BF9;  
 AC Q96BF9;  
 DT 01-DEC-2001 (TREMELrel. 19, Created)  
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)  
 DE Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1  
 DE antiproteinase, antitrypsin), member 1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=COLON;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR EMBL; BC015642; AAH15642.1; -.  
 DR InterPro; IPR000215; Serpin.  
 DR Pfam; PF00079; serpin; 1.  
 DR SMART; SM00093; SERPIN; 1.  
 DR PROSITE; PS00284; SERPIN; UNKNOWN\_1.  
 KW Serpin.  
 SQ SEQUENCE 418 AA; 46708 MW; FFOE525F303542AE CRC64;  
 Query Match 75.7%; Score 2026; DB 4; Length 418;  
 Best Local Similarity 99.7%; Pred. No. 5.3e-130;  
 Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 EDPOGDAQKTDTSHTDQDPTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 61  
 Db 25 EDPOGDAQKTDTSHTDQDPTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 84  
 QY 62 FAMLISLGTADTHDEILEGLNENLTHDIITKFLNEDRRSASLHLPKLSITGYDLK 121  
 Db 85 FAMLISLGTADTHDEILEGLNENLTHDIITKFLNEDRRSASLHLPKLSITGYDLK 144  
 QY 122 SEGKLVDFKLEDDVKKLHSAFTVNEGDTEAKKQINDVEGTGQKIVDLVKELDRDT 181  
 Db 145 SEGKLVDFKLEDDVKKLHSAFTVNEGDTEAKKQINDVEGTGQKIVDLVKELDRDT 204  
 QY 182 VFALVNYIFFKQKWERPEVDEEDFHVQDVTVKVPMMKRLGMFNIOHCKKLSWVL 241  
 Db 205 VFALVNYIFFKQKWERPEVDEEDFHVQDVTVKVPMMKRLGMFNIOHCKKLSWVL 264  
 QY 242 LMKYLGNTAIFFLPDGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 301  
 Db 265 LMKYLGNTAIFFLPDGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 324  
 QY 302 SVLGGLGTTKVFNSGADLSGVTEAPLKLKSAVHKAVLTIDKGTGAAGAMFLEAIPMSI 361  
 Db 325 SVLGGLGTTKVFNSGADLSGVTEAPLKLKSAVHKAVLTIDKGTGAAGAMFLEAIPMSI 384

QY 362 PPEVKFNKPFVFLMIEQNTKSPFLMGKVVNPQK 395  
 Db 385 PPEVKFNKPFVFLMIEQNTKSPFLMGKVVNPQK 418  
 RESULT 3  
 Q00394 PRELIMINARY; PRT; 396 AA.  
 ID Q00394;  
 AC Q00394;  
 DT 01-JUL-1997 (TREMELrel. 04, Created)  
 DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)  
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
 DE Alpha-1-antitrypsin (Fragment).  
 GN PI.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RA Yoshida K., Suzuki Y., Yamamoto K., Watanabe M., Sinohara H.;  
 RT "Cloning and sequencing of complementary DNAs encoding alpha-2-HS  
 RT glycoprotein, alpha-1-antitrypsin, and beta-actin from african green  
 RT monkey, Cercopithecus aethiops."  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RX MEDLINE=85026667; PubMed=633329;  
 RA Colau B., Chuchana P., Bollen A.;  
 RT "Revised sequence of full-length complementary DNA coding for human  
 RT alpha 1-antitrypsin."  
 RL DNA 3:327-330(1984).  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR EMBL; AB004044; BAA20264.1; -.  
 DR HSSP; P01009; 9API.  
 DR InterPro; IPR000215; Serpin.  
 DR Pfam; PF00079; serpin; 1.  
 DR SMART; SM00093; SERPIN; 1.  
 DR PROSITE; PS00284; SERPIN; 1.  
 KW Serpin.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 396 AA; 44587 MW; 1042EABFAA0A2825 CRC64;  
 Query Match 71.3%; Score 1908; DB 6; Length 396;  
 Best Local Similarity 92.9%; Pred. No. 5.4e-122;  
 Matches 367; Conservative 19; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 MEDPOGDAQKTDTSHTDQDPTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIAT 60  
 Db 2 VEDPOGDAQKTDTSHTDQDPTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIAT 61  
 QY 61 AFAMLISLGTADTHDEILEGLNENLTHDIITKFLNEDRRSASLHLPKLSITGYDLK 120  
 Db 62 AFAMLISLGTADTHDEILEGLNENLTHDIITKFLNEDRRSASLHLPKLSITGYDLK 121  
 QY 121 LSEGLKLVDFKLEDDVKKLHSAFTVNEGDTEAKKQINDVEGTGQKIVDLVKELDRD 180  
 Db 122 LNKSVKVVDFKLEDDVKKLHSAFTVNEGDTEAKKQINDVEGTGQKIVDLVKELDRD 181  
 QY 181 TVFALVNYIFFKQKWERPEVDEEDFHVQDVTVKVPMMKRLGMFNIOHCKKLSWVL 240  
 Db 182 TVFALVNYIFFKQKWERPEVDEEDFHVQDVTVKVPMMKRLGMFNIOHCKKLSWVL 241  
 QY 241 LLMKYLGNATAIFFLPDGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 300  
 Db 242 LLMKYLGNATAIFFLPDGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 301  
 QY 301 KSVLGGLGTTKVFNSGADLSGVTEAPLKLKSAVHKAVLTIDKGTGAAGAMFLEAIPMS 360  
 Db 325 SVLGGLGTTKVFNSGADLSGVTEAPLKLKSAVHKAVLTIDKGTGAAGAMFLEAIPMS 384

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Db 302 KTVLGHGKITKVFNSGADLSGVTEDAPLKSKAVHKAVLTIDEKGTAAAGAMFLEAIPMS 361
QY 361 IPPEVKFNKPFVFLMTEQNTKSPLEMGKVVNPQK 395
Db 362 IPPEVKFNKPFVFLMTEQNTKSPLEMGKVVNPQK 396

RESULT 4
O54761 PRELIMINARY; PRT; 413 AA.
AC O54761;
DT 01-JUN-1998 (TremBLrel. 06, Created)
DT 01-JUN-1998 (TremBLrel. 06, Last sequence update)
DE Alpha-antitrypsin-like protein.
OS Sperophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scluridae; Sciurinae;
OC Sperophilus.
OX NCBI_TaxID=43179;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=98094263; PubMed=9434174;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uenatsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RT "Expression of multiple alphas-1-antitrypsin-like genes in hibernating
RT species of the squirrel family.";
RL Gene 204:127-132(1997).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AB000550; BAA24420.1; -.
DR HSSP; P01009; IOLP.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
SQ SEQUENCE 413 AA; 45953 MW; B08D2544695EE0F4 CRC64;

Query Match 55.0%; Score 1470; DB 11; Length 413;
Best Local Similarity 71.9%; Pred. No. 3.8e-91;
Matches 277; Conservative 54; Mismatches 54; Indels 0; Gaps 0;

QY 9 AOKTDTSHHDDHPTFNKITPNLAFAFSLYRQLAHQSNSTNFIFFSPVSTATAPAMLSLG 68
Db 27 AQETGASKHDOEHPASHRAPNLAFAFSLYRVLAHESNTNFIFFSPVSTATAMALASLSLG 86
QY 69 TKADTHDEILGLNFTLPEAOIHGEGFQELRLTNQPSQLQTTGNGLFLUSEGLKV 128
Db 87 TKADTHQIMGLGNFTLPTAESDIHGQFQHLQLTLNKNPSQLQTTGNGLFDHNLKLL 146
QY 129 DKFLVDYKLYHSAFTVNFQDTEEAQKQINDYVEKGTQGIKIVDLVKELDRDTVFALVNY 188
Db 147 DKFLQDVKNLYHSAFTDFTNTEEAQKQINTYVEKGTQGIKIVDLVKELDRDVSVALVNY 206
QY 189 IFFGKWERPEVKDTEEDFHVQDVTTVKVPMMKRLGMFNIHQCKKLSWVLMKYLGN 248
Db 207 IFFGKWERPEVKDTEEDFHVQDVTTVKVPMMKRLGMFNIHQCKKLSWVLMKYLGN 266
QY 249 ATAFILPDECKLQHLNELTHDITTKFLENERDRSASLHPLKSLTGTVDLSVGLQGLG 308
Db 267 ATAFILPDECKLQHLNELTHDITTKFLENERDRSASLHPLKSLTGTVDLSVGLQGLG 326
QY 309 ITKVFNSGADLSGVTEAPLKSKAVHKAVLTIDEKGTAAAGAMFLEAIPMSIPPEVKEN 368
Db 327 ITNVSFKADLSGTTEDPLRVSQLHKAHLTIDERGTEAAGATFLEMPSPPEVKFD 386
QY 369 KPFVFLMTEQNTKSPLEMGKVVNPQK 393
Db 387 KPELWIIHSTKSPLEMGKVVNPQK 411

RESULT 5

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O46519

ID O46519 PRELIMINARY; PRT; 421 AA.

AC O46519;

DT 01-JUN-1998 (TremBLrel. 06, Created)

DT 01-JAN-1999 (TremBLrel. 09, Last sequence update)

DE Alpha-1-antitrypsin.

GN SPI2.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI\_TaxID=9796;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ARABIAN BREED;

RA Giffard J.M., Irvin Z.V., Bell T.K., Brandon R.B.;

RT "Equine alpha-1-antitrypsin gene.";

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

DR EMBL; AF034077; AAC83412.1; -.

DR HSSP; P01009; 1KCT.

DR InterPro; IPR000215; Serpin.

DR Pfam; PF00079; serpin; 1.

DR SMART; SM00093; SERPIN; 1.

DR PROSITE; PS00284; SERPIN; 1.

KW Serpin.

SQ SEQUENCE 421 AA; 46942 MW; D79B101312AC8259 CRC64;

Query Match 54.7%; Score 1462.5; DB 6; Length 421;

Best Local Similarity 70.0%; Pred. No. 1.3e-91;

Matches 278; Conservative 53; Mismatches 63; Indels 3; Gaps 1;

QY 2 EDPOGDAAKTDTSHHDDH---PTFNKITPNLAFAFSLYRQLAHQSNSTNFIFFSPVSI 58

Db 25 EDLQGCVAQQTATHAHDDEHLQEPAEHKIAPNLADFAFSLYRHVAHQSNNTNFIFFSPVSI 84

QY 59 ATAFAMLSLGTAKADTHDEILGLNFTLPEAOIHGEGFQELRLTNQPSQLQTTGNG 118

Db 85 ATAFALLSLGAKGDTHTQILEGLSFLNTELAQAIDHGFQHLNLAHSDNQLQTTGNG 144

QY 119 LFLSEGLKIVDKFLEDVKKLYHSAFTVNFQDTEEAQKQINDYVEKGTQGIKIVDLVKELD 178

Db 145 LFDIESAKLLDKFLEDVKKLYHSAFISINPROTEEAQKQINDYVEKGTQGIKIVDLVKELD 204

QY 179 RDTFVALVNYIPFGKWERPEVKDTEEDFHVQDVTTVKVPMMKRLGMFNIHQCKKLS 238

Db 205 KDTVLALVNYIEFGKWERPEVTEQDFHVDKTTVVRVPMHRLSSFDVQYSDTLSS 264

QY 239 WVLLMKYLGNAATAIFPLPDGKLOHLENELTHDITTKFLENERDRSASLHPLKSLTGT 298

Db 265 WVLLLDYAGNATAFFLDPQGLQHLDELTLTKGILARFLGNRHSSFVNVVHLPKLSISGT 324

QY 299 DLKSVLGQLGITKVFNSGADLSGVTEAPLKSKAVHKAVLTIDEKGTAAAGAMFLEAIP 358

Db 325 DLTSILPELGITKVFNSRQADLSGITEEVLTVSKALHKAHLTIDEKGTAAAGTTWWEIMP 384

QY 359 MSIPPEVKFNKPFVFLMTEQNTKSPLEMGKVVNPQK 395

Db 385 ISLPPDLKFNRPVFLIYDNTKSPLEMGKVVNPQK 421

RESULT 6

P97277

ID P97277 PRELIMINARY; PRT; 413 AA.

AC P97277;

DT 01-MAY-1997 (TremBLrel. 03, Created)

DT 01-MAY-1997 (TremBLrel. 03, Last sequence update)

DE Alpha-1-antitrypsin precursor.

OS Mesocricetus auratus (Golden hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Mesocricetus.

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OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96004896; PubMed=7548212;
RA Nakatani T., Suzuki Y., Yoshida K., Shinohara H.;
RL "Molecular cloning and sequence analysis of cDNA encoding plasma
RT alpha-1-antiprotease from Syrian hamster: implications for the
RT evolution of rodentia.";
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; D49709; BAA08557.1; -.
DR HSP; P01009; 9API.
DR InterPro; IPR00215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
KW Serpin; Signal.
FT SIGNAL 1 24
FT CHAIN 25 413
FT SEQUENCE 413 AA; 45819 MW; 71D192E106A1EB36 CRC64;
Query Match 54.1%; Score 1446.5; DB 11; Length 413;
Best Local Similarity 70.8%; Pred. No. 1.5e-90;
Matches 274; Conservative 54; Mismatches 58; Indels 1; Gaps 1;
QY 9 AOKTDSHHDDHPTFNKIPNLAEFAFSLYROLAHSNSTNIFPSVSIATAFAMLSLG 68
DB 27 AQETDASKDQEHQACCKIAPNLADSFNLYRELHQSNNTNIFPSVSIATAFAMLSLG 86
QY 69 TKADTHDEILEGLNFNLTEIPEAQIHGEOELLRTLNQPSQLQTLTGNGFLSEGLKLV 128
DB 87 TKGVTHTQILEGLGNLTETAEAEVHKPHNLQTNRPDNLQTLTGNGFLTHNNLKV 146
QY 129 DKFLEDVKLYHSEAFVNFQDTEEAQKQINDYVEKGTQGIYDLVKELDRDTVFALVNY 188
DB 147 DKFLEEVKNYHSEAFVNFQDTEEAQKQINGEVEKGTQGIYDLVKELDRDTVFALVNY 206
QY 189 IFFKGKWERPEVKDTEEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWVLLMKYLGN 248
DB 207 IFFKGKWKPFADNTEADFHVDKTTTVKVPMMKRLGMFNVHVTSLSSWVLLMDYLG 266
QY 249 ATAFILPDEGKLOHLENEHTHDIITKFLNEDRRSASLHLPKLSITGYDLKSVLGOLG 308
DB 267 ATAFILPDEGKMOHLEQTLNKEIGKFLKDRHTRSANVHLPKLSISGTYNKLALDPLG 326
QY 309 ITKVFSGADLSGVTEAPLKLKAVHKAVALTIDEGTEAAGAMFLEAIPMSIPPEVKFN 368
DB 327 SPFTAIIVDRQTAQSPFLFGKVVNPQT 413
RESULT 7
Q64118
ID Q64118 PRELIMINARY; PRT; 406 AA.
AC Q64118;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Alpha-1-antiprotease.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95152268; PubMed=7852275;
RA Goto K., Suzuki Y., Yoshida K., Yamamoto K., Shinohara H.;
RL "Plasma alpha-1-antiprotease from the Mongolian gerbil, Meriones
RT unguiculatus: isolation, partial characterization, sequencing of cDNA,

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RT and implications for molecular evolution.";
RL J. Biochem. 116:582-588(1994).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; S77822; BAB33367.1; -.
DR HSP; P01009; IOLP.
DR InterPro; IPR00215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
KW Serpin.
SQ SEQUENCE 406 AA; 45126 MW; 814613E44C7AA469 CRC64;
Query Match 51.4%; Score 1374; DB 11; Length 406;
Best Local Similarity 68.7%; Pred. No. 1.3e-85;
Matches 265; Conservative 56; Mismatches 59; Indels 6; Gaps 2;
QY 9 AOKTDSHHDDHPTFNKIPNLAEFAFSLYROLAHSNSTNIFPSVSIATAFAMLSLG 68
DB 27 AEKTDSSH--QDH---IMASNLADFAFLYRVLSHOSNTNIFLPLSLATAMLSLG 80
QY 69 TKADTHDEILEGLNFNLTEIPEAQIHGEOELLRTLNQPSQLQTLTGNGFLSEGLKLV 128
DB 81 SKDDTKAQLLOGLHNLTESETADHKGFOHLLKTLNRPDNLQTLTGSSLFVNNSLV 140
QY 129 DKFLEDVKLYHSEAFVNFQDTEEAQKQINDYVEKGTQGIYDLVKELDRDTVFALVNY 188
DB 141 EKFELEVKNYHSEAFVNFADSEAKKTINSFVEKATHGKIVDLVKLEIDTIVLAVNY 200
QY 189 IFFKGKWERPEVKDTEEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWVLLMKYLGN 248
DB 201 IFFKGKWKPFDPPELTEADFHVDKTTTVKVPMMKRLGMFNVHVTSLSSWVLLMDYLG 260
QY 249 ATAFILPDEGKLOHLENEHTHDIITKFLNEDRRSASLHLPKLSITGYDLKSVLGOLG 308
DB 261 ATAFILPDEGKMOHLEQTLNKEIYKFLQNRHTRSANVHLPKLSISGTYNKLKVLSPG 320
QY 309 ITKVFSGADLSGVTEAPLKLKAVHKAVALTIDEGTEAAGAMFLEAIPMSIPPEVKFN 368
DB 321 ITQVFSNGADLSGTTDVPKLSKAVHKAVALTIDEGTEAAGTTVLEAVPMSIPPEVKFN 380
QY 369 KPFFVFLMIEQNTKSPFLFGKVVNPQT 394
DB 381 NPFVVICDKKHTQSPFLFGKVVNPQT 406
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Q28665
ID Q28665 PRELIMINARY; PRT; 413 AA.
AC Q28665;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alpha-1-antiprotease E precursor.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95251597; PubMed=7733871;
RA Saito A., Shinohara H.;
RL "Rabbit alpha-1-antiprotease E: a novel recombinant serpin which
RT does not inhibit proteinases.";
RL Biochem. J. 307:369-375(1995).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; D17725; BAA04579.1; -.
DR HSP; P01009; 8API.
DR InterPro; IPR00215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin; Signal.
FT SIGNAL 1 23
FT CHAIN 24 413
FT POTENTIAL.
FT ALPHA-1-ANTIPROTEINASE E.

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ID Q91XC1 PRELIMINARY; PRT; 425 AA.  
 AC Q91XC1;  
 DT 01-DEC-2001 (TremBLrel. 19, Created)  
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)  
 DE Unknown (Protein for IMAGE:4210562) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR EMBL; BC010988; AAH10988.1; -.  
 DR InterPro; IPR000215; Serpin.  
 DR Pfam; PF00079; serpin; 1.  
 DR PROSITE; PS00284; SERPIN; UNKNOWN\_1.  
 KW Serpin.  
 FT NON\_TER  
 SQ SEQUENCE 425 AA; 47157 MW; EA9E50E40C33CAFC CRC64;  
  
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 Best Local Similarity 64.6%; Pred. No. 1.4e-82;  
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 QY 10 QKTDTSHHDDHPTFNKTPNLAFAFSLYRQLAHQSNSTNIFSPVSIATAFAMLSIGT 69  
 Db 40 QETDTSQKDS-PASHEIATNLGDEAFSLYRELVLHQSNSTNIFSPVSIATAFAMLSIGS 98  
  
 QY 70 KADTHDEILGLNLFNLTEIPAQIHEGFQELLRTLNQPSQLQTLTGNGFLSEGLKLV 129  
 Db 99 KGDTHQILEGQFNLTOTSEADIIKSFQHLQLTLNRPDSELSQLSTGNGFLVFNNDKLVE 158  
  
 QY 130 KLEVDKLYLHSEAFVNFQDTEEAQINDYVEKGTGKIVDLVKELDRDTVFALVNI 189  
 Db 159 KLEEAKNHYQAEVSNFAESEAQKVINDEVEKGTGKTAQVAVKLLDQDTVFALANI 218  
  
 QY 190 FPKGKWRPFVKKDEEDFHVDQVTVTKVPMKRLGMFNTOHCKKLSWLLMKYLQNA 249  
 Db 219 LFKGKWKPFDPENTEEAEFHVDESTTVKVPMTLSGMLDVHHCSTLSSWLLMDYAGNA 278  
  
 QY 250 TAIFFLPDGLQHLNELTHDIITKFLNEDRRSASLHLPKLSITCTYDLKSVLQGLI 309  
 Db 279 TAVFLPDGKMQHLEQTLSEKLSKFLNRRRLAQIHFPRLSISGEYNLKTLMSPILGI 338  
  
 QY 310 TKVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEKGTAAAGAMPLEAIPMSIPVEKFN 368  
 Db 339 TRIFNNGADLSGITEENAPLKLSQAVHKAVLTIDETGTEAAATVLLAVPYSMPPILRFD 398  
  
 QY 369 KPFVFLMIDQNTKSPFLMGKVVNPTOK 395  
 Db 399 HPFLFIPEHTQSPFLGVGVVDPTHK 425  
  
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 Q07298  
 ID Q07298 PRELIMINARY; PRT; 413 AA.  
 AC Q07298;  
 DT 01-NOV-1996 (TremBLrel. 01, Created)  
 DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
 DE Alpha-1-antitrypsinase S-1 precursor.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93293795; PubMed=8514734;  
 RA Saito A., Sinohara H.;

RT "Rabbit plasma alpha-1-antitrypsinase S-1: cloning, sequencing,  
 RT expression, and proteinase inhibitory properties of recombinant  
 RT protein.";  
 RL J. Biochem. 113:456-461(1993).  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR EMBL; D16104; BAA03678.1; -.  
 DR HSP; P01009; BAP1.  
 DR InterPro; IPR000215; Serpin.  
 DR Pfam; PF00079; serpin; 1.  
 DR SMART; SM00093; SERPIN; 1.  
 DR PROSITE; PS00284; SERPIN; UNKNOWN\_1.  
 KW Serpin; Signal.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 413 ALPHA-1-ANTITRYPSINASE S-1.  
 SQ SEQUENCE 413 AA; 45749 MW; 75C6004D6C7190BA CRC64;  
  
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 Best Local Similarity 65.2%; Pred. No. 2.9e-82;  
 Matches 253; Conservative 58; Mismatches 77; Indels 0; Gaps 0;  
  
 QY 7 DAAQKTDTSHHDDHPTFNKTPNLAFAFSLYRQLAHQSNSTNIFSPVSIATAFAMLS 66  
 Db 25 DEAQETAVSSHEQDHPACHRIAPSLAEFALSLYREVAHESNTNIFSPVSIATAFAMLS 84  
  
 QY 67 LGTKADTHDEILGLNLFNLTEIPAQIHEGFQELLRTLNQPSQLQTLTGNGFLSEGLK 126  
 Db 85 LGAKGDTHQVLEGLKFNLTETAEAQIHDFGRHLLHVTNRPDSELSQLAAGNALVWHENLK 144  
  
 QY 127 LVDFKLEVDKLYLHSEAFVNFQDTEEAQINDYVEKGTGKIVDLVKELDRDTVFALV 186  
 Db 145 LQHKLEDAKLYQSEAFVDFRDPDQAKTKINSHVEKGTGKIVDLVQLDARTLLALV 204  
  
 QY 187 NYIFFKGRWPFVKKDEEDFHVDQVTVTKVPMKRLGMFNTOHCKKLSWLLMKYL 246  
 Db 205 NYVFFKGRWPFVKKDEEDFHVDQVTVTKVPMKRLGMFNTOHCKKLSWLLMKYL 264  
  
 QY 247 GNATFELPDGKMQHLEQTLSEKLSKFLNRRRLAQIHFPRLSISGEYNLKTLMSPILGI 306  
 Db 265 GNATFELPDGKMQHLEQTLSEKLSKFLNRRRLAQIHFPRLSISGEYNLKTLMSPILGI 324  
  
 QY 307 LGITKVSNGADLSGVTEE-APLKLSKAVHKAVLTIDEKGTAAAGAMPLEAIPMSIPVEK 366  
 Db 325 LGITQVSDNADLSGITEEQEPKLVQSLHAKAVLTIDERGTEAAGATVGTGIMPSSLPESVI 384  
  
 QY 367 FNKPFVFLMIDQNTKSPFLMGKVVNPTQ 394  
 Db 385 FDRPFLFVYSHKLSPLFVGKVVDPDQ 412  
  
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 Q8VC41  
 ID Q8VC41 PRELIMINARY; PRT; 413 AA.  
 AC Q8VC41;  
 DT 01-MAR-2002 (TremBLrel. 20, Created)  
 DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)  
 DE Similar to serine protease inhibitor 1-4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RA Strausberg R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC021850; AAH21850.1; -.  
 DR InterPro; IPR000215; Serpin.  
 DR Pfam; PF00079; serpin; 1.  
 DR SMART; SM00093; SERPIN; 1.  
 DR PROSITE; PS00284; SERPIN; UNKNOWN\_1.  
 KW Protease.  
 SQ SEQUENCE 413 AA; 45995 MW; C96A4ECO7951872 CRC64;

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Query Match          49.5%; Score 1324; DB 11; Length 413;
Best Local Similarity 64.3%; Pred. No. 3.3e-82;
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QY 10 QKDTSHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGT 69
Db :||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
28 QETDTSQKDS-PASHEIATNLGDFAIRLYRELHVQSNSTNIFFSPVSIATAFAMLSLGS 86
QY 70 KADTHDEILEGINFNLTPEAQIHEGFOELLRTLNQPDQSOLOLTTGNGFLSEGLKLYD 129
Db :||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
87 KGDTHQTILEGLQFNLTQTAEDIHKSQHLQLTLNRPDSELQSLSTGNGFLFVNNDKLVE 146
QY 130 KPLEDVKKLYHSEAFVNFQDTEAKKINDYVEKGTQGIKIVDLVKELDRDTVFALVNYI 189
Db :||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
147 KFELEAKHYQAEVFSVNFASEAKKVINDFVEKGTQGIKIVEAVKELDQDTVFALANYI 206
QY 190 PFKGKWERPFEVKDTEEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNA 249
Db :||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
207 LFKGKWKQFPDPENTEEAEFHVDESTTVKVPMMTSLGMLDVHHCSSLSSWVLLMDYVGNT 266
QY 250 TAIFPLPDEGKLOHLENLTHDIITKLENEEDRRSASLHLPKLSITGTIDYDLKSVLGOIGI 309
Db :||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
267 TAVFLPDGDKMQHLEQTLNKLKSLKLLNRRHSDAQIHPPRLSIGNYNLKTLMSPLGI 326
QY 310 TKVFSNGADLSGVTEE-APLKLKSAVHKAVLTIDEKGTAAAGAMFLEAIPMSIPPEVKFN 368
Db :||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
327 TRIFNNGADLSGITEENAPLKLKSAVHKAVLTIDETGTEAAAATVLOAATYSMPPIIRFD 386
QY 369 KPFVFLMIEQNTKSLPFMGKVVNPTQK 395
Db :||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
387 HPFLFIIEEHSQSPLFVGKVVDPTHK 413

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